==========

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2007; month=12; day=31; hr=11; min=48; sec=34; ms=931;]

==========

Validated By CRFValidator v 1.0.3

Application No: 10566944 Version No: 2.1

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 300	Invalid codon found Ile SEQID (1) POS: 97
E 300	Invalid codon found Glu SEQID (1) POS: 100
E 300	Invalid codon found Asn SEQID (1) POS: 103
E 300	Invalid codon found Tyr SEQID (1) POS: 106
E 300	Invalid codon found Gln SEQID (1) POS: 109
E 300	Invalid codon found Gly SEQID (1) POS: 112
E 300	Invalid codon found Arg SEQID (1) POS: 115
E 300	Invalid codon found Asp SEQID (1) POS: 118
E 300	Invalid codon found Ala SEQID (1) POS: 121
E 300	Invalid codon found Thr SEQID (1) POS: 124
E 300	Invalid codon found Asp SEQID (1) POS: 127
E 300	Invalid codon found Ala SEQID (1) POS: 130
E 300	Invalid codon found Phe SEQID (1) POS: 133
E 300	Invalid codon found Met SEQID (1) POS: 136
E 300	Invalid codon found Val SEQID (1) POS: 139
E 300	Invalid codon found Met SEQID (1) POS: 142
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code	Error Description
E 300	Invalid codon found Leu SEQID (1) POS: 481
E 300	Invalid codon found Val SEQID (1) POS: 484
E 300	Invalid codon found Gly SEQID (1) POS: 487
E 300	Invalid codon found Leu SEQID (1) POS: 490 This error has occured more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code		Error Description
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (26)
W	402	Undefined organism found in <213> in SEQ ID (29)
W	402	Undefined organism found in <213> in SEQ ID (30)

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code		Error Description
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W	402	Undefined organism found in <213> in SEQ ID (33)
W	402	Undefined organism found in <213> in SEQ ID (34)
W	402	Undefined organism found in <213> in SEQ ID (35)
W	402	Undefined organism found in <213> in SEQ ID (36)
W	402	Undefined organism found in <213> in SEQ ID (41)
W	402	Undefined organism found in <213> in SEQ ID (42)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (42)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (46)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (58)
W	402	Undefined organism found in <213> in SEQ ID (67)
W	402	Undefined organism found in <213> in SEQ ID (68)
W	402	Undefined organism found in <213> in SEQ ID (69)
W	402	Undefined organism found in <213> in SEQ ID (70)
W	402	Undefined organism found in <213> in SEQ ID (71)
W	402	Undefined organism found in <213> in SEQ ID (72)
W	402	Undefined organism found in <213> in SEQ ID (73)
W	402	Undefined organism found in <213> in SEQ ID (74)

This error has occured more than 20 times, will not be displayed

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (115)
W	213	Artificial or Unknown found in <213> in SEQ ID (116)
W	213	Artificial or Unknown found in <213> in SEQ ID (121)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (121)
W	213	Artificial or Unknown found in <213> in SEQ ID (122)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (122)
W	213	Artificial or Unknown found in <213> in SEQ ID (123)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (123)
W	213	Artificial or Unknown found in <213> in SEQ ID (124)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (124)
W	213	Artificial or Unknown found in <213> in SEQ ID (125)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (125)
W	213	Artificial or Unknown found in <213> in SEQ ID (126)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (126)
W	213	Artificial or Unknown found in <213> in SEQ ID (127)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (127)
W	213	Artificial or Unknown found in <213> in SEQ ID (128)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (128)
W	213	Artificial or Unknown found in <213> in SEQ ID (129)

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code		Error Description
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (129)
W	213	Artificial or Unknown found in <213> in SEQ ID (130)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (130)
W	213	Artificial or Unknown found in <213> in SEQ ID (139)
W	213	Artificial or Unknown found in <213> in SEQ ID (140)
W	213	Artificial or Unknown found in <213> in SEQ ID (141)
W	213	Artificial or Unknown found in <213> in SEQ ID (142)
W	213	Artificial or Unknown found in <213> in SEQ ID (143)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (143)
W	213	Artificial or Unknown found in <213> in SEQ ID (144)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (144)
W	213	Artificial or Unknown found in <213> in SEQ ID (145)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (145)
W	213	Artificial or Unknown found in <213> in SEQ ID (146) This error has occured more than 20 times, will not be displayed
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (146)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (147)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (148)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (149)

Input Set:

Output Set:

Started: 2007-12-31 11:47:29.794
Finished: 2007-12-31 11:47:48.193
Elapsed: 0 hr(s) 0 min(s) 18 sec(s) 399 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

Error code		Error Description
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (150)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (151)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (152) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Zank, Thorsten
Bauer, Jorg
Cirpus, Petra
Abbadi, Amine
Heinz, Ernst
Qiu, Xiao
Vrinten, Patricia
Sperling, Petra
Domergue, Frederic
Meyer, Astrid
Kirsch, Jelena

<120> METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY ACIDS IN TRANSGENIC ORGANISMS

<130> 12810-00193-US

<140> 10/566,944
<141> 2006-02-01

<150> DE 103 35 992.3
<151> 2003-08-01

<150> DE 103 44 557.9
<151> 2003-09-24

<150> DE 103 47 869.8
<151> 2003-10-10

<150> DE 103 59 593.7
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<150> DE 10 2004 009 457.8
<151> 2004-02-27

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<170> PatentIn version 3.1

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<223> delta8-desaturase

<400> 1

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atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca        48
Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
1               5                  10                  15

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att        96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
            20                  25                  30

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg       144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met

        35                  40                  45

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat       192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
    50                  55                  60

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag       240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65                  70                  75                  80

gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat       288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
                85                  90                  95

gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt       336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
            100                 105                 110

gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att       384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
        115                 120                 125

ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct       432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
    130                 135                 140

cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac       480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145                 150                 155                 160

ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca       528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr

                165                 170                 175

tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa       576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
            180                 185                 190

ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag       624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
        195                 200                 205

gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc       672
```

```
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
    210                 215                 220

cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg      720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
225                 230                 235                 240

tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac      768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
                245                 250                 255

caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg      816
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
            260                 265                 270

cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc      864
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
        275                 280                 285

ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc      912
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe


    290                 295                 300

ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
305                 310                 315                 320

ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat     1008
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
                325                 330                 335

gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga     1056
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
            340                 345                 350

ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc     1104
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
        355                 360                 365

cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag     1152
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
    370                 375                 380

cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc     1200
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
385                 390                 395                 400

ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc     1248
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
                405                 410                 415

gcg ggg aag gct cta taa                                            1266
Ala Gly Lys Ala Leu

            420
```

<210> 2
<211> 421
<212> PRT
<213> Euglena gracilis

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
180 185 190

```
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
        195                 200                 205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
    210                 215                 220

Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
225                 230                 235                 240

Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
                245                 250                 255

Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
            260                 265                 270

His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
        275                 280                 285

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
    290                 295                 300

Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
305                 310                 315                 320

Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
                325                 330                 335

Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
            340                 345                 350

Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
        355                 360                 365

His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
    370                 375                 380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
385                 390                 395                 400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
                405                 410                 415

Ala Gly Lys Ala Leu
```

420

<210> 3
<211> 777
<212> DNA
<213> Isochrysis galbana

<220>
<221> CDS
<222> (1)..(777)
<223> delta9-elongase

<400> 3

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atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc       48
Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1               5                  10                  15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg       96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
            20                  25                  30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg      144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
        35                  40                  45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg      192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
    50                  55                  60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc      240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65                  70                  75                  80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag      288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
                85                  90                  95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag      336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
            100                 105                 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg      384
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
        115                 120                 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat      432
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
    130                 135                 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg      480
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145                 150                 155                 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc      528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
                165                 170                 175
```

```
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg      576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
            180                 185                 190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc      624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
        195                 200                 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct      672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
    210                 215                 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt      720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
225                 230                 235                 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag      768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
                245                 250                 255

cag ctc tag                                                         777
Gln Leu
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<210> 4
<211> 258
<212> PRT
<213> Isochrysis galbana

<400> 4

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Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1               5                   10                  15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
            20                  25                  30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
        35                  40                  45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
    50                  55                  60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65                  70                  75                  80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
                85                  90                  95
```

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
130 135 140

Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145 150 155 160

Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
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Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
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Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
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Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
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Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
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gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt       96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
            20                  25                  30

ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat      144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
        35                  40                  45

gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt      192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
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ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat      240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
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acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gt
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